

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/257,272DATE: 04/12/1999  
TIME: 09:10:16

INPUT SET: S31419.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: HU, JING-SHAN  
ROSEN, CRAIG A.  
CAO, LIANG

(ii) TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

(iii) NUMBER OF SEQUENCES: 15

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
(B) STREET: 1100 NEW YORK AVENUE  
(C) CITY: WASHINGTON  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/257,272  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/999,811  
(B) FILING DATE:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/465,968  
(B) FILING DATE: 06-JUN-1995

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MARKOWICZ, KAREN R.  
(B) REGISTRATION NUMBER: 36,351  
(C) REFERENCE/DOCKET NUMBER: 1488.1000004

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47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: (202)371-2600  
49 (B) TELEFAX: (202)371-2540  
50  
51  
52

53 (2) INFORMATION FOR SEQ ID NO:1:  
54

55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 1674 base pairs  
57 (B) TYPE: nucleic acid  
58 (C) STRANDEDNESS: double  
59 (D) TOPOLOGY: linear  
60

61 (ii) MOLECULE TYPE: cDNA  
62  
63

64 (ix) FEATURE:  
65 (A) NAME/KEY: sig\_peptide  
66 (B) LOCATION: 12..80  
67

68 (ix) FEATURE:  
69 (A) NAME/KEY: mat\_peptide  
70 (B) LOCATION: 81..1268  
71

72 (ix) FEATURE:  
73 (A) NAME/KEY: CDS  
74 (B) LOCATION: 12..1268  
75  
76

77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
78

79	GTCCTTCCAC C ATG CAC TCG CTG GGC TTC TTC TCT GTG GCG TGT TCT CTG	50
80	Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu	
81	-23 -20 -15	
82		
83	CTC GCC GCT GCG CTG CTC CCG GGT CCT CGC GAG GCG CCC GCC GCC GCC	98
84	Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala	
85	-10 -5 1 5	
86		
87	GCC GCC TTC GAG TCC GGA CTC GAC CTC TCG GAC GCG GAG CCC GAC GCG	146
88	Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala	
89	10 15 20	
90		
91	GGC GAG GCC ACG GCT TAT GCA AGC AAA GAT CTG GAG GAG CAG TTA CGG	194
92	Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg	
93	25 30 35	
94		
95	TCT GTG TCC AGT GTA GAT GAA CTC ATG ACT GTA CTC TAC CCA GAA TAT	242
96	Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr	
97	40 45 50	
98		
99	TGG AAA ATG TAC AAG TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC	290

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100	Trp	Lys	Met	Tyr	Lys	Cys	Gln	Leu	Arg	Lys	Gly	Gly	Trp	Gln	His	Asn	
101	55					60					65					70	
102																	
103	AGA	GAA	CAG	GCC	AAC	CTC	AAC	TCA	AGG	ACA	GAA	GAG	ACT	ATA	AAA	TTT	338
104	Arg	Glu	Gln	Ala	Asn	Leu	Asn	Ser	Arg	Thr	Glu	Glu	Thr	Ile	Lys	Phe	
105					75				80						85		
106																	
107	GCT	GCA	GCA	CAT	TAT	AAT	ACA	GAG	ATC	TTG	AAA	AGT	ATT	GAT	AAT	GAG	386
108	Ala	Ala	Ala	His	Tyr	Asn	Thr	Glu	Ile	Leu	Lys	Ser	Ile	Asp	Asn	Glu	
109				90					95					100			
110																	
111	TGG	AGA	AAG	ACT	CAA	TGC	ATG	CCA	CGG	GAG	GTG	TGT	ATA	GAT	GTG	GGG	434
112	Trp	Arg	Lys	Thr	Gln	Cys	Met	Pro	Arg	Glu	Val	Cys	Ile	Asp	Val	Gly	
113			105					110					115				
114																	
115	AAG	GAG	TTT	GGA	GTC	GCG	ACA	AAC	ACC	TTC	TTT	AAA	CCT	CCA	TGT	GTG	482
116	Lys	Glu	Phe	Gly	Val	Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	
117		120					125					130					
118																	
119	TCC	GTC	TAC	AGA	TGT	GGG	GGT	TGC	TGC	AAT	AGT	GAG	GGG	CTG	CAG	TGC	530
120	Ser	Val	Tyr	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Ser	Glu	Gly	Leu	Gln	Cys	
121	135					140					145					150	
122																	
123	ATG	AAC	ACC	AGC	ACG	AGC	TAC	CTC	AGC	AAG	ACG	TTA	TTT	GAA	ATT	ACA	578
124	Met	Asn	Thr	Ser	Thr	Ser	Tyr	Leu	Ser	Lys	Thr	Leu	Phe	Glu	Ile	Thr	
125					155					160					165		
126																	
127	GTG	CCT	CTC	TCT	CAA	GGC	CCC	AAA	CCA	GTA	ACA	ATC	AGT	TTT	GCC	AAT	626
128	Val	Pro	Leu	Ser	Gln	Gly	Pro	Lys	Pro	Val	Thr	Ile	Ser	Phe	Ala	Asn	
129				170					175					180			
130																	
131	CAC	ACT	TCC	TGC	CGA	TGC	ATG	TCT	AAA	CTG	GAT	GTT	TAC	AGA	CAA	GTT	674
132	His	Thr	Ser	Cys	Arg	Cys	Met	Ser	Lys	Leu	Asp	Val	Tyr	Arg	Gln	Val	
133			185					190					195				
134																	
135	CAT	TCC	ATT	ATT	AGA	CGT	TCC	CTG	CCA	GCA	ACA	CTA	CCA	CAG	TGT	CAG	722
136	His	Ser	Ile	Ile	Arg	Arg	Ser	Leu	Pro	Ala	Thr	Leu	Pro	Gln	Cys	Gln	
137		200					205					210					
138																	
139	GCA	GCG	AAC	AAG	ACC	TGC	CCC	ACC	AAT	TAC	ATG	TGG	AAT	AAT	CAC	ATC	770
140	Ala	Ala	Asn	Lys	Thr	Cys	Pro	Thr	Asn	Tyr	Met	Trp	Asn	Asn	His	Ile	
141	215					220					225					230	
142																	
143	TGC	AGA	TGC	CTG	GCT	CAG	GAA	GAT	TTT	ATG	TTT	TCC	TCG	GAT	GCT	GGA	818
144	Cys	Arg	Cys	Leu	Ala	Gln	Glu	Asp	Phe	Met	Phe	Ser	Ser	Asp	Ala	Gly	
145					235					240					245		
146																	
147	GAT	GAC	TCA	ACA	GAT	GGA	TTC	CAT	GAC	ATC	TGT	GGA	CCA	AAC	AAG	GAG	866
148	Asp	Asp	Ser	Thr	Asp	Gly	Phe	His	Asp	Ile	Cys	Gly	Pro	Asn	Lys	Glu	
149				250					255					260			
150																	
151	CTG	GAT	GAA	GAG	ACC	TGT	CAG	TGT	GTC	TGC	AGA	GCG	GGG	CTT	CGG	CCT	914
152	Leu	Asp	Glu	Glu	Thr	Cys	Gln	Cys	Val	Cys	Arg	Ala	Gly	Leu	Arg	Pro	

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153	265	270	275	
154				
155	GCC AGC TGT GGA CCC CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT			962
156	Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys			
157	280	285	290	
158				
159	GTC TGT AAA AAC AAA CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA			1010
160	Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu			
161	295	300	305	310
162				
163	TTT GAT GAA AAC ACA TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA			1058
164	Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg			
165	315	320	325	
166				
167	AAT CAA CCC CTA AAT CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT			1106
168	Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser			
169	330	335	340	
170				
171	CCA CAG AAA TGC TTG TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC			1154
172	Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys			
173	345	350	355	
174				
175	AGC TGT TAC AGA CGG CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA			1202
176	Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro			
177	360	365	370	
178				
179	GGA TTT TCA TAT AGT GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG			1250
180	Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp			
181	375	380	385	390
182				
183	CAA AGA CCA CAA ATG AGC TAAGATTGTA CTGTTTTCCA GTTCATCGAT			1298
184	Gln Arg Pro Gln Met Ser			
185	395			
186				
187	TTTCTATTAT GGAAACTGT GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG			1358
188				
189	TGGGTCCATG CTAACAAAGA CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA			1418
190				
191	GAAATGGACT GGAGCTCATC TGCAAAAGGC CTCTTGTAAG GACTGGTTTT CTGCCAATGA			1478
192				
193	CCAAACAGCC AAGATTTTCC TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT			1538
194				
195	CCACTAAAAA TATTGTTTCT GCATTCATTT TTATAGCAAC AACAAATTGGT AAAACTCACT			1598
196				

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**SEQUENCE VERIFICATION REPORT**  
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Original Text